

SPNT

interference search

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	30	(lysophosphatidic adj acid adj acyltransferase).clm. or lpaat.clm. or (1-acyl adj sn-glycerol-3-phosphate adj acyltransferase).clm.	US-PGPUB; USPAT	OR	OFF	2005/07/07 12:36
L2	15	l1 and (polypeptide.clm. or (amino adj acid adj sequence).clm.)	US-PGPUB; USPAT	OR	OFF	2005/07/07 12:37

STIC-Biotech/ChemLib

157022

From: Steadman, David (AU1652)
Sent: Monday, June 20, 2005 2:26 PM
To: STIC-Biotech/ChemLib
Subject: 10/667,494 sequence search request

NAME: David Steadman
AU: 1652
Date: 06/20/05
Office: Remsen 2B05
Mailbox: Remsen 2C70

Please perform the following search or searches in commercial and interference databases:

- 1) Standard search of SEQ ID NO:13 against nucleic acid databases. Please provide 30 results or hits rather than the standard 15.
- 2) Standard search of SEQ ID NO:13 against amino acid databases. Please provide 30 results or hits rather than the standard 15.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Patent Examiner
Art Unit 1652 - Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 2C70
(571) 272-0942

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2005, 17:03:13 ; Search time 4327 Seconds
(without alignments)
4210.576 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=90
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb_in:*
4: gb_om:*
5: gb_ov:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	1999	100.0	1333	9	AB040138	AB040138 Homo sapi

4	1999	100.0	1577	9	BC011971	BC011971 Homo sapi
5	1999	100.0	1660	6	BD265488	BD265488 Mammalian
6	1999	100.0	1660	6	AR370494	AR370494 Sequence
7	1999	100.0	1660	6	AR442693	AR442693 Sequence
8	1999	100.0	1660	9	AF156774	AF156774 Homo sapi
9	1999	100.0	1960	6	AX317982	AX317982 Sequence
10	1999	100.0	2377	9	BC063552	BC063552 Homo sapi
11	1999	100.0	2397	9	BC040603	BC040603 Homo sapi
12	1995	99.8	1128	6	AX239832	AX239832 Sequence
13	1995	99.8	1832	6	AX239824	AX239824 Sequence
14	1910.5	95.6	3060	6	AX376270	AX376270 Sequence
15	1910.5	95.6	3060	6	AX697228	AX697228 Sequence
16	1910.5	95.6	3060	9	AY358704	AY358704 Homo sapi
17	1895	94.8	1153	10	AY167588	AY167588 Mus muscu
18	1888	94.4	3378	10	BC058519	BC058519 Mus muscu
19	1888	94.4	3379	10	BC052382	BC052382 Mus muscu
20	1855	92.8	1769	6	AR339350	AR339350 Sequence
21	1789.5	89.5	1523	6	BD265489	BD265489 Mammalian
22	1789.5	89.5	1523	6	AR370495	AR370495 Sequence
23	1789.5	89.5	1523	6	AR442694	AR442694 Sequence
24	1789.5	89.5	1523	9	AF156775	AF156775 Homo sapi
25	1694	84.7	4208	5	BC081052	BC081052 Xenopus l
26	1685	84.3	2728	5	BC081323	BC081323 Xenopus t
27	1685	84.3	3509	5	BC043776	BC043776 Xenopus l
28	1681.5	84.1	3955	6	CQ842883	CQ842883 Sequence
29	1681.5	84.1	3955	9	AK125804	AK125804 Homo sapi
30	1561	78.1	5633	6	BD183432	BD183432 Novel gen
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32	1387	69.4	3878	6	AX211367	AX211367 Sequence
33	1353	67.7	1540	5	BC071000	BC071000 Xenopus l
34	1329	66.5	1082	5	CR385377	CR385377 Gallus ga
35	1301	65.1	1943	5	BC056788	BC056788 Danio rer
36	1289	64.5	1137	6	AX119047	AX119047 Sequence
37	1289	64.5	1721	9	BC020209	BC020209 Homo sapi
38	1289	64.5	1771	6	AX135548	AX135548 Sequence
39	1289	64.5	1774	6	BD265490	BD265490 Mammalian
40	1289	64.5	1774	6	AR370496	AR370496 Sequence
41	1289	64.5	1774	6	AR442695	AR442695 Sequence
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43	1289	64.5	1781	6	AR252488	AR252488 Sequence
44	1289	64.5	1781	6	AR528661	AR528661 Sequence
45	1289	64.5	1781	6	AX056649	AX056649 Sequence
46	1289	64.5	1781	6	AX403268	AX403268 Sequence
47	1289	64.5	1781	6	AX464286	AX464286 Sequence
48	1289	64.5	1781	9	AY358506	AY358506 Homo sapi
49	1289	64.5	1794	6	AX135587	AX135587 Sequence
50	1289	64.5	1824	9	HSA420473	AJ420473 Homo sapi
51	1281	64.1	1869	10	BC047281	BC047281 Mus muscu
52	1280	64.0	1868	10	AB067572	AB067572 Rattus no
53	1279	64.0	1847	9	AK074208	AK074208 Homo sapi
54	1173	58.7	1245	5	BX929790	BX929790 Gallus ga
55	1047	52.4	1229	6	CQ725794	CQ725794 Sequence
56	932	46.6	697	5	BX933055	BX933055 Gallus ga
c 57	832.5	41.6	231097	5	AC146542	AC146542 Gasterost
58	771	38.6	882	9	HSA227890	AJ227890 Homo sapi
59	764.5	38.2	1241	6	CQ581799	CQ581799 Sequence
60	764.5	38.2	1623	3	BT001546	BT001546 Drosophil
61	738	36.9	693	6	AX526051	AX526051 Sequence
62	705.5	35.3	870	9	HSA227891	AJ227891 Homo sapi
63	679.5	34.0	1215	6	CQ581829	CQ581829 Sequence
64	679.5	34.0	1586	3	AY070622	AY070622 Drosophil
65	636	31.8	5822	6	CQ581798	CQ581798 Sequence
66	636	31.8	171907	2	AC116538	AC116538 Drosophil
c 67	636	31.8	186795	3	AC010660	AC010660 Drosophil
c 68	636	31.8	279904	3	AE003527	AE003527 Drosophil
c 69	635	31.8	6391	2	AC020478	AC020478 Drosophil
70	630	31.5	1702	6	BD224793	BD224793 Novel pla
71	625	31.3	1176	8	AY616009	AY616009 Brassica
72	620	31.0	1615	8	BNLPAAT	Z95637 B.napus mRN
73	617	30.9	1170	6	BD224663	BD224663 Novel pla
74	612.5	30.6	1515	6	A52744	A52744 Sequence 3

	75	612.5	30.6	1515	6	AR349252	AR349252 Sequence
	76	612	30.6	1480	8	AY084461	AY084461 Arabidops
	77	609.5	30.5	1486	8	LDAGPATMR	Z48730 L.douglasii
c	78	608.5	30.4	156469	2	AC046149	AC046149 Mus muscu
	79	606	30.3	4074	6	CQ581828	CQ581828 Sequence
c	80	606	30.3	4077	2	AC020479	AC020479 Drosophil
	81	603.5	30.2	1415	8	BT009239	BT009239 Triticum
	82	596	29.8	1514	6	A38840	A38840 Sequence 1
	83	596	29.8	1514	6	AR062686	AR062686 Sequence
	84	596	29.8	1514	6	AR135355	AR135355 Sequence
	85	596	29.8	1518	8	ZMIAG3PAT	Z29518 Z.mays (Bla
	86	588.5	29.4	159108	10	AC009295	AC009295 Mus muscu
c	87	562.5	28.1	242445	2	AC119100	AC119100 Rattus no
c	88	562.5	28.1	260515	2	AC130089	AC130089 Rattus no
	89	547.5	27.4	2861	6	CQ612428	CQ612428 Sequence
	90	538.5	26.9	1396	8	AF213937	AF213937 Prunus du

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2005, 17:01:53 ; Search time 573 Seconds
(without alignments)
3884.507 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Command line parameters:
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1999	100.0	1333	3	AAA71493	Aaa71493 Human lys
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3	1999	100.0	1660	3	AAA51068	Aaa51068 Human LPA
4	1999	100.0	1660	6	AAD24423	Aad24423 Human LPA

5	1999	100.0	1660	9	ABX16124	Abx16124 Human cDN
6	1999	100.0	1660	12	ADJ93796	Adj93796 Human lys
7	1999	100.0	1660	12	ADN49480	Adn49480 Human lys
8	1999	100.0	1660	12	ADO04619	Ado04619 Human lys
9	1999	100.0	1660	13	ACN40851	Acn40851 Tumour-as
10	1999	100.0	1960	6	AAD24014	Aad24014 Human dru
11	1995	99.8	1832	5	AAH75152	Aah75152 Nucleotid
12	1995	99.8	1832	12	ADQ15077	Adq15077 Human can
13	1995	99.8	1832	13	ADR40140	Adr40140 Human lys
14	1992	99.6	1629	6	ABL55080	Abl55080 Human cDN
15	1910.5	95.6	3059	4	AAS46093	Aas46093 Human DNA
16	1910.5	95.6	3060	3	AAA37104	Aaa37104 Human PRO
17	1910.5	95.6	3060	4	AAF54413	Aaf54413 Primer #8
18	1910.5	95.6	3060	8	ACA89543	Aca89543 cDNA enco
19	1910.5	95.6	3060	8	ACA73553	Aca73553 Human sec
20	1910.5	95.6	3060	8	ACA05868	Aca05868 Human sec
21	1910.5	95.6	3060	8	ACA66702	Aca66702 cDNA enco
22	1910.5	95.6	3060	8	ACF20277	Acf20277 Human sec
23	1910.5	95.6	3060	8	ACF19663	Acf19663 Human sec
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25	1910.5	95.6	3060	8	ACF13116	Acf13116 Human sec
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43	1910.5	95.6	3060	8	ACD14072	Acd14072 Human PRO
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45	1910.5	95.6	3060	8	ACC88597	Acc88597 Human sec
46	1910.5	95.6	3060	8	ACD21337	Acd21337 Human sec
47	1910.5	95.6	3060	8	ABX75709	Abx75709 Human cDN
48	1910.5	95.6	3060	8	ABX97912	Abx97912 Human PRO
49	1910.5	95.6	3060	8	ACA97388	Aca97388 Novel hum
50	1910.5	95.6	3060	8	ACA57851	Aca57851 Human PRO
51	1910.5	95.6	3060	8	ACD14379	Acd14379 Human PRO
52	1910.5	95.6	3060	8	ACC91162	Acc91162 Human sec
53	1910.5	95.6	3060	8	ACC88904	Acc88904 Human sec
54	1910.5	95.6	3060	8	ACD07101	Acd07101 Human PRO
55	1910.5	95.6	3060	8	ACA67552	Aca67552 Human PRO
56	1910.5	95.6	3060	8	ACC81607	Acc81607 Human sec
57	1910.5	95.6	3060	8	ACC89211	Acc89211 Human sec
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59	1910.5	95.6	3060	8	ACC89825	Acc89825 Human sec
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66	1910.5	95.6	3060	8	ACA70807	Aca70807 Human sec
67	1910.5	95.6	3060	8	ACA95317	Aca95317 Novel hum
68	1910.5	95.6	3060	8	ACC86260	Acc86260 Human sec
69	1910.5	95.6	3060	8	ACC90132	Acc90132 Human sec
70	1910.5	95.6	3060	8	ACD12740	Acd12740 Human sec
71	1910.5	95.6	3060	8	ACF19970	Acf19970 Human sec
72	1910.5	95.6	3060	8	ABX76914	Abx76914 Human PRO
73	1910.5	95.6	3060	8	ACA73246	Aca73246 Novel hum
74	1910.5	95.6	3060	8	ACA68789	Aca68789 Novel hum
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76	1910.5	95.6	3060	8	ACA70500	Aca70500	Human	sec
77	1910.5	95.6	3060	8	ACD14686	Acd14686	Human	PRO
78	1910.5	95.6	3060	8	ACA68358	Aca68358	Novel	hum
79	1910.5	95.6	3060	8	ABX98823	Abx98823	Novel	hum
80	1910.5	95.6	3060	8	ACC81300	Acc81300	Human	sec
81	1910.5	95.6	3060	8	ACA95624	Aca95624	Novel	hum
82	1910.5	95.6	3060	8	ACD04542	Acd04542	Novel	hum
83	1910.5	95.6	3060	8	ACC87983	Acc87983	Human	sec
84	1910.5	95.6	3060	8	ACF12645	Acf12645	Human	sec
85	1910.5	95.6	3060	8	ACA96360	Aca96360	Human	PRO
86	1910.5	95.6	3060	8	ACA65134	Aca65134	Human	PRO
87	1910.5	95.6	3060	8	ACA73860	Aca73860	Human	sec
88	1910.5	95.6	3060	8	ACA74272	Aca74272	Novel	hum
89	1910.5	95.6	3060	8	ACA96667	Aca96667	Human	PRO
90	1910.5	95.6	3060	8	ACD10773	Acd10773	cDNA	enco

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2005, 17:09:00 ; Search time 207 Seconds
(without alignments)
2972.174 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=na.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=90 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667494@cgn_1_1_105@runat_24062005_160313_295 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1999	100.0	1660	3	US-09-215-252-12	Sequence 12, Appl
	2	1999	100.0	1660	4	US-09-970-989A-12	Sequence 12, Appl
	3	1855	92.8	1769	4	US-09-620-312D-841	Sequence 841, App
	4	1789.5	89.5	1523	3	US-09-215-252-14	Sequence 14, Appl
	5	1789.5	89.5	1523	4	US-09-970-989A-14	Sequence 14, Appl
	6	1289	64.5	1774	3	US-09-215-252-16	Sequence 16, Appl
	7	1289	64.5	1774	4	US-09-970-989A-16	Sequence 16, Appl
	8	612.5	30.6	1515	4	US-08-818-581B-3	Sequence 3, Appli
	9	596	29.8	1514	2	US-08-454-267-1	Sequence 1, Appli
	10	596	29.8	1514	2	US-08-941-319-1	Sequence 1, Appli
	11	596	29.8	1514	3	US-09-035-098-1	Sequence 1, Appli

12	266	13.3	458	4	US-09-513-999C-2079	Sequence 2079, Ap
13	247	12.4	271	4	US-09-513-999C-10074	Sequence 10074, A
14	243	12.2	1763	4	US-09-620-312D-637	Sequence 637, App
15	242	12.1	1409	3	US-09-338-907-72	Sequence 72, Appl
16	242	12.1	1409	3	US-09-338-907-184	Sequence 184, App
17	242	12.1	1409	3	US-09-218-207-72	Sequence 72, Appl
18	242	12.1	1409	3	US-09-218-207-184	Sequence 184, App
19	240	12.0	5227	2	US-08-996-306-3	Sequence 3, Appli
20	240	12.0	5245	3	US-09-338-907-3	Sequence 3, Appli
21	240	12.0	5245	3	US-09-218-207-3	Sequence 3, Appli
22	234	11.7	5250	3	US-09-338-907-69	Sequence 69, Appl
23	234	11.7	5250	3	US-09-218-207-69	Sequence 69, Appl
24	228	11.4	5290	3	US-09-338-907-119	Sequence 119, App
25	228	11.4	5290	3	US-09-218-207-119	Sequence 119, App
26	203.5	10.2	5326	3	US-09-338-907-124	Sequence 124, App
27	203.5	10.2	5326	3	US-09-218-207-124	Sequence 124, App
28	195.5	9.8	5148	3	US-09-338-907-112	Sequence 112, App
29	195.5	9.8	5148	3	US-09-218-207-112	Sequence 112, App
30	186	9.3	5234	3	US-09-338-907-113	Sequence 113, App
31	186	9.3	5234	3	US-09-218-207-113	Sequence 113, App
c 32	178.5	8.9	1629	4	US-09-252-991A-13111	Sequence 13111, A
33	177	8.9	5044	3	US-09-338-907-115	Sequence 115, App
34	177	8.9	5044	3	US-09-218-207-115	Sequence 115, App
35	174.5	8.7	969	4	US-09-252-991A-12688	Sequence 12688, A
36	174.5	8.7	1041	4	US-09-252-991A-12831	Sequence 12831, A
37	174.5	8.7	4958	3	US-09-338-907-116	Sequence 116, App
38	174.5	8.7	4958	3	US-09-218-207-116	Sequence 116, App
39	173	8.7	775	4	US-09-220-132-191	Sequence 191, App
40	170	8.5	5020	3	US-09-338-907-120	Sequence 120, App
41	170	8.5	5020	3	US-09-218-207-120	Sequence 120, App
42	161.5	8.1	960	4	US-09-540-236-1906	Sequence 1906, Ap
c 43	161.5	8.1	31940	4	US-09-596-002-13	Sequence 13, Appl
44	159	8.0	557	4	US-09-270-767-15072	Sequence 15072, A
45	152	7.6	1095	4	US-09-252-991A-5981	Sequence 5981, Ap
46	152	7.6	1200	4	US-09-252-991A-5964	Sequence 5964, Ap
c 47	152	7.6	1515	4	US-09-252-991A-5909	Sequence 5909, Ap
48	148.5	7.4	966	4	US-09-328-352-1604	Sequence 1604, Ap
49	147.5	7.4	963	4	US-09-489-039A-3247	Sequence 3247, Ap
50	142	7.1	5100	3	US-09-338-907-122	Sequence 122, App
51	142	7.1	5100	3	US-09-218-207-122	Sequence 122, App
52	134.5	6.7	5057	3	US-09-338-907-123	Sequence 123, App
53	134.5	6.7	5057	3	US-09-218-207-123	Sequence 123, App
54	125	6.3	3244	2	US-08-321-670-1	Sequence 1, Appli
55	112.5	5.6	1008	4	US-09-248-796A-7206	Sequence 7206, Ap
56	109.5	5.5	3969	4	US-09-949-016-437	Sequence 437, App
57	104	5.2	3967	4	US-09-949-016-2730	Sequence 2730, Ap
58	100	5.0	801	4	US-09-248-796A-1458	Sequence 1458, Ap
59	97.5	4.9	927	4	US-09-252-991A-2499	Sequence 2499, Ap
60	96.5	4.8	795	4	US-09-902-540-6455	Sequence 6455, Ap
c 61	96.5	4.8	12865	4	US-09-902-540-1048	Sequence 1048, Ap
62	95	4.8	983	4	US-09-270-767-2263	Sequence 2263, Ap
63	95	4.8	983	4	US-09-270-767-17545	Sequence 17545, A
c 64	94.5	4.7	26659	4	US-09-902-540-1237	Sequence 1237, Ap
65	94	4.7	276237	4	US-09-949-016-17504	Sequence 17504, A
c 66	92.5	4.6	640681	4	US-09-790-988-1	Sequence 1, Appli
67	92	4.6	1245	4	US-09-543-681A-3922	Sequence 3922, Ap
68	91	4.6	696	4	US-09-902-540-4831	Sequence 4831, Ap
69	91	4.6	1146	4	US-09-107-433-520	Sequence 520, App
70	91	4.6	1203	4	US-09-583-110-2419	Sequence 2419, Ap
71	90	4.5	1408	1	US-08-254-404-21	Sequence 21, Appl
72	90	4.5	1408	2	US-08-327-451E-21	Sequence 21, Appl
73	90	4.5	1408	2	US-08-458-109-21	Sequence 21, Appl
74	90	4.5	1470	4	US-09-559-622-2	Sequence 2, Appli
75	90	4.5	1470	4	US-09-559-622-6	Sequence 6, Appli
76	89.5	4.5	570	4	US-09-107-532A-2249	Sequence 2249, Ap
c 77	89	4.5	21526	4	US-09-949-016-14685	Sequence 14685, A
c 78	89	4.5	194714	4	US-09-949-016-11869	Sequence 11869, A
c 79	89	4.5	196714	4	US-09-949-016-15474	Sequence 15474, A
c 80	88	4.4	4846	4	US-08-956-171E-276	Sequence 276, App
c 81	88	4.4	4846	4	US-08-781-986A-276	Sequence 276, App
82	87.5	4.4	1045	2	US-08-458-109-42	Sequence 42, Appl

83	87.5	4.4	1146	2	US-08-458-109-41	Sequence 41, Appl
84	87.5	4.4	1511	4	US-09-949-016-3463	Sequence 3463, Ap
85	87.5	4.4	1522	4	US-09-949-016-855	Sequence 855, App
86	87.5	4.4	2562	4	US-09-620-312D-1047	Sequence 1047, Ap
87	87.5	4.4	3190	4	US-09-949-016-5219	Sequence 5219, Ap
88	87.5	4.4	31602	4	US-09-949-016-16961	Sequence 16961, A
89	87.5	4.4	56516	2	US-08-996-306-1	Sequence 1, Appli
90	87.5	4.4	56516	3	US-09-338-907-1	Sequence 1, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2005, 18:29:19 ; Search time 624 Seconds
(without alignments)
3766.337 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10667494/runat_24062005_160314_378/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=na.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=90 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10667494_@CGN_1_1_723_@runat_24062005_160314_378
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1999	100.0	1660	9	US-09-970-989-12	Sequence 12, Appl
2	1999	100.0	1660	18	US-10-667-494-12	Sequence 12, Appl
3	1999	100.0	1660	18	US-10-667-462-12	Sequence 12, Appl
4	1999	100.0	1660	18	US-10-667-464-12	Sequence 12, Appl
5	1999	100.0	1960	17	US-10-296-606-22	Sequence 22, Appl
6	1995	99.8	1128	9	US-09-798-029-13	Sequence 13, Appl
7	1995	99.8	1832	9	US-09-798-029-5	Sequence 5, Appli
8	1995	99.8	1832	20	US-10-737-450-35	Sequence 35, Appl
9	1995	99.8	1832	21	US-10-772-636-21	Sequence 21, Appl
10	1910.5	95.6	3060	10	US-09-946-374-296	Sequence 296, App
11	1910.5	95.6	3060	13	US-10-052-586-337	Sequence 337, App
12	1910.5	95.6	3060	14	US-10-174-590-337	Sequence 337, App
13	1910.5	95.6	3060	14	US-10-176-758-337	Sequence 337, App
14	1910.5	95.6	3060	14	US-10-175-737-337	Sequence 337, App
15	1910.5	95.6	3060	14	US-10-174-581-337	Sequence 337, App
16	1910.5	95.6	3060	14	US-10-176-483-337	Sequence 337, App
17	1910.5	95.6	3060	14	US-10-176-749-337	Sequence 337, App
18	1910.5	95.6	3060	14	US-10-176-914-337	Sequence 337, App
19	1910.5	95.6	3060	14	US-10-176-915-337	Sequence 337, App
20	1910.5	95.6	3060	14	US-10-173-706-337	Sequence 337, App
21	1910.5	95.6	3060	14	US-10-175-738-337	Sequence 337, App
22	1910.5	95.6	3060	14	US-10-175-752-337	Sequence 337, App
23	1910.5	95.6	3060	14	US-10-176-482-337	Sequence 337, App
24	1910.5	95.6	3060	14	US-10-176-757-337	Sequence 337, App
25	1910.5	95.6	3060	14	US-10-176-913-337	Sequence 337, App
26	1910.5	95.6	3060	14	US-10-180-552-337	Sequence 337, App
27	1910.5	95.6	3060	14	US-10-180-557-337	Sequence 337, App
28	1910.5	95.6	3060	14	US-10-173-700-337	Sequence 337, App
29	1910.5	95.6	3060	14	US-10-174-572-337	Sequence 337, App
30	1910.5	95.6	3060	14	US-10-174-579-337	Sequence 337, App
31	1910.5	95.6	3060	14	US-10-174-582-337	Sequence 337, App
32	1910.5	95.6	3060	14	US-10-174-588-337	Sequence 337, App
33	1910.5	95.6	3060	14	US-10-175-739-337	Sequence 337, App
34	1910.5	95.6	3060	14	US-10-175-740-337	Sequence 337, App
35	1910.5	95.6	3060	14	US-10-175-743-337	Sequence 337, App
36	1910.5	95.6	3060	14	US-10-176-488-337	Sequence 337, App
37	1910.5	95.6	3060	14	US-10-176-492-337	Sequence 337, App
38	1910.5	95.6	3060	14	US-10-176-747-337	Sequence 337, App
39	1910.5	95.6	3060	14	US-10-176-750-337	Sequence 337, App
40	1910.5	95.6	3060	14	US-10-176-985-337	Sequence 337, App
41	1910.5	95.6	3060	14	US-10-176-987-337	Sequence 337, App
42	1910.5	95.6	3060	14	US-10-176-992-337	Sequence 337, App
43	1910.5	95.6	3060	14	US-10-176-993-337	Sequence 337, App
44	1910.5	95.6	3060	14	US-10-184-658-337	Sequence 337, App
45	1910.5	95.6	3060	14	US-10-176-991-337	Sequence 337, App
46	1910.5	95.6	3060	14	US-10-173-695-337	Sequence 337, App
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48	1910.5	95.6	3060	14	US-10-173-705-337	Sequence 337, App
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50	1910.5	95.6	3060	14	US-10-174-585-337	Sequence 337, App
51	1910.5	95.6	3060	14	US-10-174-586-337	Sequence 337, App
52	1910.5	95.6	3060	14	US-10-175-747-337	Sequence 337, App
53	1910.5	95.6	3060	14	US-10-176-481-337	Sequence 337, App
54	1910.5	95.6	3060	14	US-10-176-485-337	Sequence 337, App
55	1910.5	95.6	3060	14	US-10-176-487-337	Sequence 337, App
56	1910.5	95.6	3060	14	US-10-176-493-337	Sequence 337, App
57	1910.5	95.6	3060	14	US-10-176-756-337	Sequence 337, App
58	1910.5	95.6	3060	14	US-10-176-911-337	Sequence 337, App
59	1910.5	95.6	3060	14	US-10-176-919-337	Sequence 337, App
60	1910.5	95.6	3060	14	US-10-176-925-337	Sequence 337, App
61	1910.5	95.6	3060	14	US-10-176-978-337	Sequence 337, App
62	1910.5	95.6	3060	14	US-10-179-510-337	Sequence 337, App

63	1910.5	95.6	3060	14	US-10-180-543-337	Sequence 337, App
64	1910.5	95.6	3060	14	US-10-180-544-337	Sequence 337, App
65	1910.5	95.6	3060	14	US-10-180-546-337	Sequence 337, App
66	1910.5	95.6	3060	14	US-10-180-547-337	Sequence 337, App
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70	1910.5	95.6	3060	14	US-10-181-000-337	Sequence 337, App
71	1910.5	95.6	3060	14	US-10-183-010-337	Sequence 337, App
72	1910.5	95.6	3060	14	US-10-183-012-337	Sequence 337, App
73	1910.5	95.6	3060	14	US-10-184-614-337	Sequence 337, App
74	1910.5	95.6	3060	14	US-10-184-623-337	Sequence 337, App
75	1910.5	95.6	3060	14	US-10-184-635-337	Sequence 337, App
76	1910.5	95.6	3060	14	US-10-184-637-337	Sequence 337, App
77	1910.5	95.6	3060	14	US-10-184-646-337	Sequence 337, App
78	1910.5	95.6	3060	14	US-10-184-647-337	Sequence 337, App
79	1910.5	95.6	3060	14	US-10-184-652-337	Sequence 337, App
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81	1910.5	95.6	3060	14	US-10-187-596-337	Sequence 337, App
82	1910.5	95.6	3060	14	US-10-187-745-337	Sequence 337, App
83	1910.5	95.6	3060	14	US-10-187-885-337	Sequence 337, App
84	1910.5	95.6	3060	14	US-10-187-886-337	Sequence 337, App
85	1910.5	95.6	3060	14	US-10-199-464-337	Sequence 337, App
86	1910.5	95.6	3060	14	US-10-196-756-337	Sequence 337, App
87	1910.5	95.6	3060	14	US-10-176-751-337	Sequence 337, App
88	1910.5	95.6	3060	14	US-10-176-760-337	Sequence 337, App
89	1910.5	95.6	3060	14	US-10-176-990-337	Sequence 337, App
90	1910.5	95.6	3060	14	US-10-180-541-337	Sequence 337, App

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2005, 17:05:19 ; Search time 3117 Seconds
(without alignments)
4591.648 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTKQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10667494/runat_24062005_160312_280/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=na.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=90
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667494_@CGN_1_1_5180_@runat_24062005_160312_280 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1895	94.8	1319	3 AK015906	AK015906 Mus muscu
2	1895	94.8	1415	3 AK076414	AK076414 Mus muscu
3	1895	94.8	3439	3 AK075715	AK075715 Mus muscu
4	1851	92.6	3240	3 AK030607	AK030607 Mus muscu
5	1810	90.5	1558	3 AK008965	AK008965 Mus muscu
6	1681	84.1	3022	3 BC033444	BC033444 Mus muscu
7	1622	81.1	1131	9 AY419544	AY419544 Homo sapi
8	1619	81.0	5079	3 HSM804230	AL832919 Homo sapi

	9	1531	76.6	1131	9	AY419546	AY419546 Mus muscu
c	10	1434.5	71.8	986	4	BI408757	BI408757 602964646
	11	1402	70.1	971	5	BX401713	BX401713 BX401713
	12	1389	69.5	1131	9	AY419545	AY419545 Pan trogl
	13	1388	69.4	1063	4	BM459459	BM459459 AGENCOURT
	14	1365	68.3	919	5	BX325280	BX325280 BX325280
	15	1289	64.5	1137	9	AY404676	AY404676 Homo sapi
	16	1289	64.5	1690	3	CR609642	CR609642 full-leng
	17	1289	64.5	1737	3	CR615061	CR615061 full-leng
	18	1289	64.5	1756	3	CR623504	CR623504 full-leng
	19	1289	64.5	1781	3	CR615644	CR615644 full-leng
	20	1289	64.5	1786	3	CR612654	CR612654 full-leng
	21	1281	64.1	1912	3	AK005139	AK005139 Mus muscu
	22	1279	64.0	797	7	CO886199	CO886199 BovGen_14
	23	1279	64.0	1137	9	AY404678	AY404678 Mus muscu
	24	1272	63.6	985	5	BQ072125	BQ072125 AGENCOURT
	25	1265	63.3	1137	9	AY404677	AY404677 Pan trogl
	26	1260	63.0	808	5	BU126102	BU126102 603151541
	27	1245	62.3	735	6	CD350550	CD350550 UI-M-GIO-
	28	1230	61.5	762	2	BE794370	BE794370 601589550
	29	1227	61.4	2084	3	BC031179	BC031179 Mus muscu
	30	1214	60.7	879	4	BI832205	BI832205 603078568
	31	1211	60.6	738	5	BX673235	BX673235 BX673235
	32	1203	60.2	827	6	CD303142	CD303142 AGENCOURT
	33	1201	60.1	1133	3	CR621965	CR621965 full-leng
	34	1192	59.6	780	5	BQ179377	BQ179377 UI-M-EWO-
	35	1176.5	58.9	923	5	BU500684	BU500684 AGENCOURT
c	36	1172.5	58.7	881	4	BI100258	BI100258 602885721
	37	1172	58.6	782	5	BP447055	BP447055 BP447055
	38	1165.5	58.3	1183	6	CD505010	CD505010 CDA71-C11
	39	1140	57.0	702	2	BB618113	BB618113 BB618113
c	40	1138	56.9	675	4	BM675712	BM675712 UI-E-EJ1-
	41	1137	56.9	669	7	CO432267	CO432267 UI-M-HXO-
	42	1135.5	56.8	1107	4	BM563288	BM563288 AGENCOURT
	43	1124	56.2	653	7	CN793611	CN793611 4128663 B
	44	1120	56.0	656	2	AW411232	AW411232 fh11b04.x
	45	1119.5	56.0	1024	4	BG424827	BG424827 602453477
	46	1106	55.3	834	7	CF217172	CF217172 AGENCOURT
	47	1105	55.3	619	7	CV023393	CV023393 321 Full
	48	1090	54.5	703	4	BG995044	BG995044 MR4-HT105
	49	1090	54.5	906	5	BQ731678	BQ731678 AGENCOURT
	50	1080	54.0	976	5	BU840364	BU840364 AGENCOURT
	51	1075	53.8	871	7	CR565259	CR565259 CR565259
	52	1071	53.6	648	2	AW410448	AW410448 fh06c04.x
	53	1070	53.5	637	7	CF744159	CF744159 UI-M-GVO-
c	54	1063	53.2	871	7	CK773096	CK773096 961699 MA
	55	1060	53.0	780	5	BU421664	BU421664 603957261
	56	1058	52.9	622	2	BE298682	BE298682 601119489
	57	1051.5	52.6	896	4	BG541849	BG541849 602569742
	58	1038.5	52.0	780	4	BI731843	BI731843 603352263
	59	1035.5	51.8	1144	5	BQ049014	BQ049014 AGENCOURT
	60	1031	51.6	839	5	BX854713	BX854713 BX854713
	61	1029.5	51.5	918	6	BY715463	BY715463 BY715463
	62	1028	51.4	609	5	BQ355739	BQ355739 MR4-HT105
	63	1027	51.4	916	6	CA983176	CA983176 AGENCOURT
	64	1014.5	50.8	606	2	BE742623	BE742623 601575450
	65	1014	50.7	764	5	BU432878	BU432878 603221112
	66	1009	50.5	1146	7	CK025426	CK025426 AGENCOURT
	67	1005	50.3	835	7	CO927422	CO927422 AGENCOURT
	68	1003.5	50.2	7746	3	CR627395	CR627395 Homo sapi
	69	1002	50.1	594	2	BF305599	BF305599 601893430
c	70	999	50.0	913	5	BX371886	BX371886 BX371886
	71	998	49.9	606	2	BF044248	BF044248 BP250002B
c	72	994	49.7	840	7	CK772757	CK772757 961330 MA
	73	980	49.0	555	4	BG997288	BG997288 MR4-HT105
	74	966	48.3	679	4	BG427551	BG427551 602494577
	75	963	48.2	796	7	CR553622	CR553622 CR553622
	76	962	48.1	905	5	BQ712742	BQ712742 AGENCOURT
	77	959	48.0	711	1	AB046249	AB046249 AB046249
	78	958	47.9	642	4	BI475471	BI475471 fq33b10.y
	79	958	47.9	733	7	CK366650	CK366650 AGENCOURT

80	954	47.7	578	5	BM931691
c 81	947.5	47.4	824	7	CK706517
82	947	47.4	593	4	BG088853
83	947	47.4	782	5	BU535433
84	945	47.3	613	2	BE334577
85	938.5	46.9	995	6	BY708850
86	934	46.7	1031	5	BX378082
c 87	929	46.5	675	4	BG076329
88	923.5	46.2	727	7	CF520201
89	921	46.1	646	4	BI733804
c 90	920	46.0	736	4	BI289530

BM931691	UI-E-EJ1-
CK706517	ZF101-P00
BG088853	H3158D09-
BU535433	AGENCOURT
BE334577	us81a09.y
BY708850	BY708850
BX378082	BX378082
BG076329	H3158D09-
CF520201	AGENCOURT
BI733804	603351964
BI289530	UI-R-DK0-

OM protein - protein search, using sw model

Run on: June 26, 2005, 12:49:55 ; Search time 127 Seconds
(without alignments)
1145.054 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1999	100.0	376	3	AAAY96590	Aay96590 Human lys
2	1999	100.0	376	3	AAB10460	Aab10460 Human lys
3	1999	100.0	376	5	AAE15294	Aae15294 Human LPA
4	1999	100.0	376	5	AAE14446	Aae14446 Human dru
5	1999	100.0	376	6	ABG74253	Abg74253 Human LPA
6	1999	100.0	376	8	ADJ93797	Adj93797 Human lys
7	1999	100.0	376	8	ADN49481	Adn49481 Human lys
8	1999	100.0	376	8	ADO04620	Ado04620 Human lys
9	1999	100.0	376	8	ABM82301	Abm82301 Tumour-as
10	1995	99.8	376	4	AAG67124	Aag67124 Amino aci
11	1995	99.8	376	8	ADQ15078	Adq15078 Human can
12	1995	99.8	376	8	ADR40141	Adr40141 Human lys
13	1992	99.6	376	5	ABG64898	Abg64898 Human alb
14	1992	99.6	376	5	ABB77011	Abb77011 Human pro
15	1992	99.6	376	8	ADL78165	Adl78165 Albumin f
16	1902.5	95.2	368	3	AAAY99422	Aay99422 Human PRO
17	1902.5	95.2	368	4	AAB66171	Aab66171 Protein o
18	1902.5	95.2	368	4	AAU29192	Aau29192 Human PRO
19	1902.5	95.2	368	6	ABU58568	Abu58568 Human PRO
20	1902.5	95.2	368	6	ABU88116	Abu88116 Novel hum
21	1902.5	95.2	368	6	ABU84431	Abu84431 Human sec
22	1902.5	95.2	368	6	ABR66305	Abr66305 Human sec
23	1902.5	95.2	368	6	ABR65695	Abr65695 Human sec
24	1902.5	95.2	368	6	ABU99635	Abu99635 Human sec

25	1902.5	95.2	368	6	ABU82874	Abu82874	Human	PRO
26	1902.5	95.2	368	6	ABU89995	Abu89995	Novel	hum
27	1902.5	95.2	368	6	ABR68244	Abr68244	Human	sec
28	1902.5	95.2	368	6	ABU96297	Abu96297	Novel	hum
29	1902.5	95.2	368	6	ABU92728	Abu92728	Human	sec
30	1902.5	95.2	368	6	ABO08805	Abo08805	Human	sec
31	1902.5	95.2	368	6	ABO02857	Abo02857	Human	sec
32	1902.5	95.2	368	6	ABR75011	Abr75011	Human	sec
33	1902.5	95.2	368	6	ABR94773	Abr94773	Human	sec
34	1902.5	95.2	368	6	ABU85746	Abu85746	Human	PRO
35	1902.5	95.2	368	6	ABU98906	Abu98906	Novel	hum
36	1902.5	95.2	368	6	ABU98121	Abu98121	Novel	hum
37	1902.5	95.2	368	6	ABU91827	Abu91827	Novel	hum
38	1902.5	95.2	368	6	ABU89520	Abu89520	Human	PRO
39	1902.5	95.2	368	6	ABU86361	Abu86361	Human	sec
40	1902.5	95.2	368	6	ABU67574	Abu67574	Human	sec
41	1902.5	95.2	368	6	ABU80602	Abu80602	Human	PRO
42	1902.5	95.2	368	6	ABR99520	Abr99520	Human	sec
43	1902.5	95.2	368	6	ABR98910	Abr98910	Human	sec
44	1902.5	95.2	368	6	ABO16433	Abo16433	Human	sec
45	1902.5	95.2	368	6	ABR92333	Abr92333	Human	sec
46	1902.5	95.2	368	6	ABO18974	Abo18974	Human	sec
47	1902.5	95.2	368	6	ABR78395	Abr78395	Human	sec
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49	1902.5	95.2	368	6	ABO00270	Abo00270	Novel	hum
50	1902.5	95.2	368	6	ABO11602	Abo11602	Human	sec
51	1902.5	95.2	368	6	ABO02247	Abo02247	Human	sec
52	1902.5	95.2	368	6	ABU88821	Abu88821	Novel	hum
53	1902.5	95.2	368	6	ABU83516	Abu83516	Human	sec
54	1902.5	95.2	368	6	ABO06317	Abo06317	Novel	hum
55	1902.5	95.2	368	6	ABR59353	Abr59353	Human	sec
56	1902.5	95.2	368	6	ABO09415	Abo09415	Human	sec
57	1902.5	95.2	368	6	ABO19279	Abo19279	Novel	hum
58	1902.5	95.2	368	6	ABO11297	Abo11297	Human	sec
59	1902.5	95.2	368	6	ABR66915	Abr66915	Human	sec
60	1902.5	95.2	368	6	ABO16128	Abo16128	Human	sec
61	1902.5	95.2	368	6	ABO13834	Abo13834	Human	sec
62	1902.5	95.2	368	6	ABU65737	Abu65737	Human	sec
63	1902.5	95.2	368	6	ABO07585	Abo07585	Human	PRO
64	1902.5	95.2	368	6	ABO03772	Abo03772	Human	sec
65	1902.5	95.2	368	6	ABR67220	Abr67220	Human	sec
66	1902.5	95.2	368	6	ABO15823	Abo15823	Human	sec
67	1902.5	95.2	368	6	ABU56104	Abu56104	Human	sec
68	1902.5	95.2	368	6	ABU65432	Abu65432	Human	PRO
69	1902.5	95.2	368	6	ABU95377	Abu95377	Novel	hum
70	1902.5	95.2	368	6	ABU71280	Abu71280	Human	PRO
71	1902.5	95.2	368	6	ABO07890	Abo07890	Human	PRO
72	1902.5	95.2	368	6	ABR70131	Abr70131	Human	sec
73	1902.5	95.2	368	6	ABR69464	Abr69464	Human	sec
74	1902.5	95.2	368	6	ABO01605	Abo01605	Human	PRO
75	1902.5	95.2	368	6	ABU81407	Abu81407	Human	PRO
76	1902.5	95.2	368	6	ABR60204	Abr60204	Human	sec
77	1902.5	95.2	368	6	ABR67939	Abr67939	Human	sec
78	1902.5	95.2	368	6	ABR65327	Abr65327	Human	sec
79	1902.5	95.2	368	6	ABR68549	Abr68549	Human	sec
80	1902.5	95.2	368	6	ABR71961	Abr71961	Human	sec
81	1902.5	95.2	368	6	ABU85441	Abu85441	Human	PRO
82	1902.5	95.2	368	6	ABU89131	Abu89131	Human	sec
83	1902.5	95.2	368	6	ABU83211	Abu83211	Human	sec
84	1902.5	95.2	368	6	ABU95067	Abu95067	Novel	hum
85	1902.5	95.2	368	6	ABU90615	Abu90615	Novel	hum
86	1902.5	95.2	368	6	ABU84126	Abu84126	Human	sec
87	1902.5	95.2	368	6	ABU93777	Abu93777	Novel	hum
88	1902.5	95.2	368	6	ABR65022	Abr65022	Human	sec
89	1902.5	95.2	368	6	ABR68854	Abr68854	Human	sec
90	1902.5	95.2	368	6	ABO06670	Abo06670	Human	sec

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 26, 2005, 16:49:02 ; Search time 49 Seconds
(without alignments)
572.817 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVG FV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1999	100.0	376	3	US-09-215-252-13	Sequence 13, Appl
	2	1999	100.0	376	4	US-09-970-989A-13	Sequence 13, Appl
	3	1682	84.1	314	3	US-09-215-252-15	Sequence 15, Appl
	4	1682	84.1	314	4	US-09-970-989A-15	Sequence 15, Appl
	5	1289	64.5	378	3	US-09-215-252-17	Sequence 17, Appl
	6	1289	64.5	378	4	US-09-970-989A-17	Sequence 17, Appl
	7	612.5	30.6	377	4	US-08-818-581B-4	Sequence 4, Appli
	8	596	29.8	374	2	US-08-454-267-2	Sequence 2, Appli
	9	596	29.8	374	2	US-08-454-267-6	Sequence 6, Appli
	10	596	29.8	374	2	US-08-941-319-2	Sequence 2, Appli
	11	596	29.8	374	2	US-08-941-319-6	Sequence 6, Appli
	12	596	29.8	374	3	US-09-035-098-2	Sequence 2, Appli
	13	596	29.8	374	3	US-09-035-098-6	Sequence 6, Appli
	14	596	29.8	374	3	US-09-215-252-5	Sequence 5, Appli
	15	596	29.8	374	4	US-09-970-989A-5	Sequence 5, Appli
	16	588	29.4	375	4	US-08-818-581B-5	Sequence 5, Appli
	17	389.5	19.5	295	2	US-08-454-267-7	Sequence 7, Appli
	18	389.5	19.5	295	2	US-08-941-319-7	Sequence 7, Appli
	19	389.5	19.5	295	3	US-09-035-098-7	Sequence 7, Appli
	20	389.5	19.5	311	4	US-08-818-581B-6	Sequence 6, Appli
	21	266	13.3	77	4	US-09-513-999C-6156	Sequence 6156, Ap
	22	241	12.1	354	3	US-09-338-907-74	Sequence 74, Appl
	23	241	12.1	354	3	US-09-218-207-74	Sequence 74, Appl
	24	240	12.0	353	2	US-08-996-306-4	Sequence 4, Appli
	25	240	12.0	353	3	US-09-338-907-4	Sequence 4, Appli
	26	240	12.0	353	3	US-09-218-207-4	Sequence 4, Appli

27	240	12.0	364	2	US-08-996-306-5	Sequence 5, Appli
28	240	12.0	364	3	US-09-338-907-5	Sequence 5, Appli
29	240	12.0	364	3	US-09-218-207-5	Sequence 5, Appli
30	232	11.6	46	3	US-09-215-252-33	Sequence 33, Appl
31	232	11.6	46	4	US-09-970-989A-33	Sequence 33, Appl
32	187.5	9.4	228	3	US-09-338-907-70	Sequence 70, Appl
33	187.5	9.4	228	3	US-09-218-207-70	Sequence 70, Appl
34	177	8.9	291	3	US-09-338-907-127	Sequence 127, App
35	177	8.9	291	3	US-09-218-207-127	Sequence 127, App
36	174.5	8.7	261	3	US-09-338-907-128	Sequence 128, App
37	174.5	8.7	261	3	US-09-218-207-128	Sequence 128, App
38	174.5	8.7	346	4	US-09-252-991A-29402	Sequence 29402, A
39	161.5	8.1	319	4	US-09-540-236-3826	Sequence 3826, Ap
40	154	7.7	112	4	US-09-270-767-46637	Sequence 46637, A
41	152	7.6	364	4	US-09-252-991A-22552	Sequence 22552, A
42	148.5	7.4	321	4	US-09-328-352-5730	Sequence 5730, Ap
43	147.5	7.4	320	4	US-09-489-039A-10418	Sequence 10418, A
44	142	7.1	315	3	US-09-338-907-134	Sequence 134, App
45	142	7.1	315	3	US-09-218-207-134	Sequence 134, App
46	139	7.0	46	3	US-09-215-252-34	Sequence 34, Appl
47	139	7.0	46	4	US-09-970-989A-34	Sequence 34, Appl
48	134.5	6.7	300	3	US-09-338-907-135	Sequence 135, App
49	134.5	6.7	300	3	US-09-218-207-135	Sequence 135, App
50	133	6.7	23	3	US-09-215-252-29	Sequence 29, Appl
51	133	6.7	23	4	US-09-970-989A-29	Sequence 29, Appl
52	125	6.3	303	2	US-08-321-670-2	Sequence 2, Appli
53	125	6.3	303	3	US-09-215-252-3	Sequence 3, Appli
54	125	6.3	303	4	US-09-970-989A-3	Sequence 3, Appli
55	112.5	5.6	335	4	US-09-248-796A-21309	Sequence 21309, A
56	109.5	5.5	185	3	US-09-338-907-136	Sequence 136, App
57	109.5	5.5	185	3	US-09-218-207-136	Sequence 136, App
58	107.5	5.4	318	3	US-09-215-252-11	Sequence 11, Appl
59	107.5	5.4	318	4	US-09-970-989A-11	Sequence 11, Appl
60	100	5.0	266	4	US-09-248-796A-15561	Sequence 15561, A
61	97	4.9	308	4	US-09-252-991A-19070	Sequence 19070, A
62	96.5	4.8	264	4	US-09-902-540-13691	Sequence 13691, A
63	95	4.8	194	4	US-09-270-767-33892	Sequence 33892, A
64	95	4.8	194	4	US-09-270-767-49109	Sequence 49109, A
65	92	4.6	414	4	US-09-543-681A-8094	Sequence 8094, Ap
66	89.5	4.5	189	4	US-09-107-532A-5903	Sequence 5903, Ap
67	87.5	4.4	249	4	US-08-818-581B-10	Sequence 10, Appl
68	87	4.4	207	4	US-08-811-519-30	Sequence 30, Appl
69	84.5	4.2	482	1	US-07-792-885A-1	Sequence 1, Appli
70	84	4.2	278	3	US-09-400-742-8	Sequence 8, Appli
71	84	4.2	278	3	US-08-618-651A-8	Sequence 8, Appli
72	84	4.2	278	3	US-09-215-252-7	Sequence 7, Appli
73	84	4.2	278	4	US-09-970-989A-7	Sequence 7, Appli
74	84	4.2	313	4	US-09-248-796A-17933	Sequence 17933, A
75	83.5	4.2	281	4	US-08-818-581B-8	Sequence 8, Appli
76	83.5	4.2	470	4	US-09-107-532A-4517	Sequence 4517, Ap
77	83	4.2	278	4	US-09-949-016-6726	Sequence 6726, Ap
78	83	4.2	300	4	US-09-949-016-9334	Sequence 9334, Ap
79	83	4.2	472	4	US-09-902-540-11899	Sequence 11899, A
80	83	4.2	670	4	US-09-587-811A-2	Sequence 2, Appli
81	82.5	4.1	3066	3	US-08-952-127-12	Sequence 12, Appl
82	81.5	4.1	482	1	US-08-142-439A-7	Sequence 7, Appli
83	81.5	4.1	482	2	US-08-869-477-7	Sequence 7, Appli
84	81	4.1	544	4	US-09-902-540-16154	Sequence 16154, A
85	81	4.1	619	4	US-09-949-016-6308	Sequence 6308, Ap
86	80	4.0	242	2	US-08-512-955-4	Sequence 4, Appli
87	80	4.0	258	4	US-09-902-540-9996	Sequence 9996, Ap
88	80	4.0	289	4	US-09-252-991A-27680	Sequence 27680, A
89	80	4.0	551	3	US-09-138-172-2	Sequence 2, Appli
90	80	4.0	698	4	US-09-436-699C-26	Sequence 26, Appl

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OM protein - protein search, using sw model

Run on: June 26, 2005, 16:53:03 ; Search time 111 Seconds
(without alignments)
1302.613 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTKQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1999	100.0	376	9	US-09-970-989-13	Sequence 13, Appl
	2	1999	100.0	376	15	US-10-296-606-9	Sequence 9, Appli
	3	1999	100.0	376	15	US-10-667-494-13	Sequence 13, Appl
	4	1999	100.0	376	15	US-10-667-462-13	Sequence 13, Appl
	5	1999	100.0	376	15	US-10-667-464-13	Sequence 13, Appl
	6	1995	99.8	376	9	US-09-798-029-6	Sequence 6, Appli
	7	1995	99.8	376	16	US-10-737-450-36	Sequence 36, Appl
	8	1995	99.8	376	17	US-10-772-636-22	Sequence 22, Appl
	9	1992	99.6	376	11	US-09-833-245-1647	Sequence 1647, Ap
	10	1902.5	95.2	368	10	US-09-946-374-297	Sequence 297, App

11	1902.5	95.2	368	13	US-10-052-586-338	Sequence 338, App
12	1902.5	95.2	368	14	US-10-174-590-338	Sequence 338, App
13	1902.5	95.2	368	14	US-10-176-758-338	Sequence 338, App
14	1902.5	95.2	368	14	US-10-175-737-338	Sequence 338, App
15	1902.5	95.2	368	14	US-10-174-581-338	Sequence 338, App
16	1902.5	95.2	368	14	US-10-176-483-338	Sequence 338, App
17	1902.5	95.2	368	14	US-10-176-749-338	Sequence 338, App
18	1902.5	95.2	368	14	US-10-176-914-338	Sequence 338, App
19	1902.5	95.2	368	14	US-10-176-915-338	Sequence 338, App
20	1902.5	95.2	368	14	US-10-173-706-338	Sequence 338, App
21	1902.5	95.2	368	14	US-10-175-738-338	Sequence 338, App
22	1902.5	95.2	368	14	US-10-175-752-338	Sequence 338, App
23	1902.5	95.2	368	14	US-10-176-482-338	Sequence 338, App
24	1902.5	95.2	368	14	US-10-176-757-338	Sequence 338, App
25	1902.5	95.2	368	14	US-10-176-913-338	Sequence 338, App
26	1902.5	95.2	368	14	US-10-180-552-338	Sequence 338, App
27	1902.5	95.2	368	14	US-10-180-557-338	Sequence 338, App
28	1902.5	95.2	368	14	US-10-173-700-338	Sequence 338, App
29	1902.5	95.2	368	14	US-10-174-572-338	Sequence 338, App
30	1902.5	95.2	368	14	US-10-174-579-338	Sequence 338, App
31	1902.5	95.2	368	14	US-10-174-582-338	Sequence 338, App
32	1902.5	95.2	368	14	US-10-174-588-338	Sequence 338, App
33	1902.5	95.2	368	14	US-10-175-739-338	Sequence 338, App
34	1902.5	95.2	368	14	US-10-175-740-338	Sequence 338, App
35	1902.5	95.2	368	14	US-10-175-743-338	Sequence 338, App
36	1902.5	95.2	368	14	US-10-176-488-338	Sequence 338, App
37	1902.5	95.2	368	14	US-10-176-492-338	Sequence 338, App
38	1902.5	95.2	368	14	US-10-176-747-338	Sequence 338, App
39	1902.5	95.2	368	14	US-10-176-750-338	Sequence 338, App
40	1902.5	95.2	368	14	US-10-176-985-338	Sequence 338, App
41	1902.5	95.2	368	14	US-10-176-987-338	Sequence 338, App
42	1902.5	95.2	368	14	US-10-176-992-338	Sequence 338, App
43	1902.5	95.2	368	14	US-10-176-993-338	Sequence 338, App
44	1902.5	95.2	368	14	US-10-184-658-338	Sequence 338, App
45	1902.5	95.2	368	14	US-10-176-991-338	Sequence 338, App
46	1902.5	95.2	368	14	US-10-173-695-338	Sequence 338, App
47	1902.5	95.2	368	14	US-10-173-697-338	Sequence 338, App
48	1902.5	95.2	368	14	US-10-173-705-338	Sequence 338, App
49	1902.5	95.2	368	14	US-10-174-576-338	Sequence 338, App
50	1902.5	95.2	368	14	US-10-174-585-338	Sequence 338, App
51	1902.5	95.2	368	14	US-10-174-586-338	Sequence 338, App
52	1902.5	95.2	368	14	US-10-175-747-338	Sequence 338, App
53	1902.5	95.2	368	14	US-10-176-481-338	Sequence 338, App
54	1902.5	95.2	368	14	US-10-176-485-338	Sequence 338, App
55	1902.5	95.2	368	14	US-10-176-487-338	Sequence 338, App
56	1902.5	95.2	368	14	US-10-176-493-338	Sequence 338, App
57	1902.5	95.2	368	14	US-10-176-756-338	Sequence 338, App
58	1902.5	95.2	368	14	US-10-176-911-338	Sequence 338, App
59	1902.5	95.2	368	14	US-10-176-919-338	Sequence 338, App
60	1902.5	95.2	368	14	US-10-176-925-338	Sequence 338, App
61	1902.5	95.2	368	14	US-10-176-978-338	Sequence 338, App
62	1902.5	95.2	368	14	US-10-179-510-338	Sequence 338, App
63	1902.5	95.2	368	14	US-10-180-543-338	Sequence 338, App
64	1902.5	95.2	368	14	US-10-180-544-338	Sequence 338, App
65	1902.5	95.2	368	14	US-10-180-546-338	Sequence 338, App
66	1902.5	95.2	368	14	US-10-180-547-338	Sequence 338, App
67	1902.5	95.2	368	14	US-10-180-549-338	Sequence 338, App
68	1902.5	95.2	368	14	US-10-180-555-338	Sequence 338, App
69	1902.5	95.2	368	14	US-10-180-559-338	Sequence 338, App
70	1902.5	95.2	368	14	US-10-181-000-338	Sequence 338, App
71	1902.5	95.2	368	14	US-10-183-010-338	Sequence 338, App
72	1902.5	95.2	368	14	US-10-183-012-338	Sequence 338, App
73	1902.5	95.2	368	14	US-10-184-614-338	Sequence 338, App
74	1902.5	95.2	368	14	US-10-184-623-338	Sequence 338, App
75	1902.5	95.2	368	14	US-10-184-635-338	Sequence 338, App
76	1902.5	95.2	368	14	US-10-184-637-338	Sequence 338, App
77	1902.5	95.2	368	14	US-10-184-646-338	Sequence 338, App
78	1902.5	95.2	368	14	US-10-184-647-338	Sequence 338, App
79	1902.5	95.2	368	14	US-10-184-652-338	Sequence 338, App
80	1902.5	95.2	368	14	US-10-187-594-338	Sequence 338, App
81	1902.5	95.2	368	14	US-10-187-596-338	Sequence 338, App

82	1902.5	95.2	368	14	US-10-187-745-338	Sequence 338, App
83	1902.5	95.2	368	14	US-10-187-885-338	Sequence 338, App
84	1902.5	95.2	368	14	US-10-187-886-338	Sequence 338, App
85	1902.5	95.2	368	14	US-10-199-464-338	Sequence 338, App
86	1902.5	95.2	368	14	US-10-196-756-338	Sequence 338, App
87	1902.5	95.2	368	14	US-10-176-751-338	Sequence 338, App
88	1902.5	95.2	368	14	US-10-176-760-338	Sequence 338, App
89	1902.5	95.2	368	14	US-10-176-990-338	Sequence 338, App
90	1902.5	95.2	368	14	US-10-180-541-338	Sequence 338, App

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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:45:01 ; Search time 45 Seconds
(without alignments)
803.945 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						
1	647.5	32.4	376	2	D96550	hypothetical prote
2	609.5	30.5	377	2	S60478	probable 1-acyl-sn
3	596	29.8	374	2	S52645	probable 1-acyl-gl
4	394.5	19.7	310	2	T06755	probable glycerol-
5	389.5	19.5	311	2	T07936	probable glycerol-
6	376.5	18.8	393	2	B96780	hypothetical prote
7	327	16.4	350	2	T40466	probable acetyltra
8	290	14.5	397	2	S45900	probable membrane
9	239.5	12.0	396	2	S54641	probable membrane
10	227.5	11.4	918	2	T34057	hypothetical prote
11	221	11.1	344	2	T31913	hypothetical prote
12	196.5	9.8	523	2	T25998	hypothetical prote
13	191	9.6	439	2	T22689	hypothetical prote
14	172.5	8.6	304	2	B83541	probable polynucle
15	172	8.6	363	2	T20608	hypothetical prote
16	152	7.6	295	2	B83587	probable polynucle
17	147	7.4	310	2	S40808	polynucleotide ade
18	147	7.4	310	2	G86073	probable endonucle
19	147	7.4	310	2	A91227	probable endonucle
20	144	7.2	302	2	AI0950	probable acyltrans
21	139.5	7.0	294	2	D82371	probable polynucle
22	137	6.9	391	2	T15366	hypothetical prote
23	127.5	6.4	279	2	T50125	probable 1-acylgly
24	125	6.3	303	2	A48600	probable sn2-acylg
25	114.5	5.7	247	2	G72223	hypothetical prote
26	102.5	5.1	936	2	T26521	hypothetical prote
27	101.5	5.1	142	2	T29793	hypothetical prote
28	98	4.9	956	2	B71250	valine-tRNA ligase

29	97	4.9	257	2	A83645	probable acyltrans
30	95.5	4.8	408	2	S56831	probable membrane
31	92.5	4.6	955	2	F84972	valine-tRNA ligase
32	90.5	4.5	608	2	H90530	conserved hypothet
33	89.5	4.5	702	2	T39483	probable transmemb
34	88.5	4.4	285	2	T15252	hypothetical prote
35	88	4.4	247	2	A81957	1-acylglycerol-3-p
36	87	4.4	288	2	H95940	probable xanthine
37	86.5	4.3	301	2	E82440	hypothetical prote
38	86.5	4.3	1279	2	G86684	prophage pil prote
39	86	4.3	247	2	G81013	1-acyl-sn-glycerol
40	86	4.3	347	2	D71690	hypothetical prote
41	86	4.3	358	2	C86291	hypothetical prote
42	86	4.3	451	2	F75131	hypothetical prote
43	86	4.3	591	2	F69837	asparagine synthas
44	85.5	4.3	243	2	B71706	probable 1-acylgly
45	85.5	4.3	531	2	T11596	hypothetical prote
46	85.5	4.3	699	2	C97176	cation transport P
47	85	4.3	283	2	F90681	taurine dioxxygenas
48	85	4.3	283	2	B85532	taurine dioxxygenas
49	84.5	4.2	241	2	G97788	hypothetical prote
50	84.5	4.2	363	1	CBUTB	ubiquinol-cytochro
51	84.5	4.2	416	2	B88493	protein F57B9.5 [i
52	84.5	4.2	469	2	E82264	probable polysacch
53	84	4.2	752	2	G69457	ribonucleoside-dip
54	84	4.2	1693	2	T30867	Rho-guanine nucleo
55	83.5	4.2	281	2	S60477	1-acylglycerol-3-p
56	83.5	4.2	582	2	T39931	probable transcrip
57	83.5	4.2	1237	2	T46609	calcium-activated
58	83.5	4.2	1322	2	T15689	hypothetical prote
59	83	4.2	347	1	C46137	opsin, violet-sens
60	83	4.2	500	1	DERZN4	NADH2 dehydrogenas
61	83	4.2	611	2	A87326	hypothetical prote
62	83	4.2	702	2	T01763	threonine-tRNA lig
63	83	4.2	709	2	T51624	threonine-tRNA lig
64	82.5	4.1	579	2	T45237	probable transfera
65	82	4.1	473	2	D82884	glycyl-tRNA synthe
66	82	4.1	515	1	QXZM4	NADH2 dehydrogenas
67	82	4.1	853	2	D70304	hypothetical prote
68	81.5	4.1	482	2	A39285	calcitonin recepto
69	81.5	4.1	485	2	T35663	probable transmemb
70	81.5	4.1	510	2	G71365	probable carnitine
71	81.5	4.1	552	2	T24173	hypothetical prote
72	81.5	4.1	1389	2	T47796	ABC transporter-li
73	81.5	4.1	1441	1	GNVULC	M polyprotein prec
74	81	4.1	331	2	T20593	hypothetical prote
75	81	4.1	332	2	A72767	hypothetical prote
76	81	4.1	506	2	JC5678	minor core protein
77	81	4.1	519	2	S75570	apolipoprotein N-a
78	81	4.1	619	2	S29839	taurine transport
79	81	4.1	881	2	S67026	probable membrane
80	81	4.1	983	2	T19874	hypothetical prote
81	80.5	4.0	371	2	B84593	hypothetical prote
82	80.5	4.0	580	2	B70868	probable transfera
83	80	4.0	223	2	H83462	heme exporter prot
84	80	4.0	421	2	F72213	hypothetical prote
85	80	4.0	508	2	T03910	UDP-glucuronosyltr
86	80	4.0	570	4	B44282	retrovirus-related
87	80	4.0	750	2	B90137	sulfate permease [
88	79.5	4.0	253	2	B87667	ABC-2 type transpo
89	79.5	4.0	265	2	G75067	hypothetical prote
90	79.5	4.0	352	2	I50047	rhodopsin - Mexica

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OM protein - protein search, using sw model

Run on: June 26, 2005, 14:26:17 ; Search time 126 Seconds
(without alignments)
1528.109 Million cell updates/sec

Title: US-10-667-494-13
Perfect score: 1999
Sequence: 1 MGLLAFLKTQFVLHLLVGFV.....GVTEIEKGSSYGNQEFKKKE 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1999	100.0	376	1 PLCC_HUMAN	Q9nrz7 homo sapien
2	1902.5	95.2	368	2 Q6UWP6	Q6uwp6 homo sapien
3	1895	94.8	376	2 Q9D517	Q9d517 m mus muscu
4	1888	94.4	376	2 Q7TT39	Q7tt39 mus musculu
5	1694	84.7	376	2 Q66J57	Q66j57 xenopus lae
6	1685	84.3	376	2 Q66IJ5	Q66ij5 xenopus tro
7	1685	84.3	376	2 Q7ZYI1	Q7zyi1 xenopus lae
8	1681.5	84.1	392	2 Q6ZUC6	Q6zuc6 homo sapien
9	1632	81.6	307	2 Q8N3Q7	Q8n3q7 homo sapien
10	1589	79.5	314	2 Q8BST2	Q8bst2 mus musculu
11	1537.5	76.9	377	2 Q7ZWC9	Q7zwc9 brachydanio
12	1353	67.7	377	2 Q6IRA0	Q6ira0 xenopus lae
13	1301	65.1	377	2 Q6PGY2	Q6pgy2 brachydanio
14	1289	64.5	378	1 PLCD_HUMAN	Q9nrz5 h 1-acyl-sn
15	1281	64.1	378	2 Q8K4X7	Q8k4x7 m lysophosp
16	1280	64.0	378	1 PLCD_RAT	Q924s1 rattus norv
17	764.5	38.2	386	2 Q9VV51	Q9vv51 drosophila
18	761	38.1	442	2 Q7QIX2	Q7qix2 anopheles g
19	679.5	34.0	380	2 Q9VV49	Q9vv49 drosophila
20	647.5	32.4	376	2 Q9SYC8	Q9syc8 arabidopsis
21	625	31.3	391	2 Q6IWY1	Q6iwy1 brassica ol
22	620	31.0	390	2 Q9XFW4	Q9xfw4 brassica na
23	611	30.6	389	2 Q8LG50	Q8lg50 arabidopsis
24	609.5	30.5	377	2 Q40119	Q40119 limnanthes
25	596	29.8	374	2 Q41745	Q41745 zea mays (m
26	485	24.3	306	2 Q9SDN3	Q9sdn3 prunus dulc
27	394.5	19.7	310	2 Q9SVX9	Q9svx9 arabidopsis
28	392	19.6	237	2 Q7X9L2	Q7x9l2 triticum ae
29	389.5	19.5	311	2 Q39317	Q39317 brassica na
30	381.5	19.1	375	2 Q9LHN4	Q9lhn4 arabidopsis

31	380.5	19.0	378	2	Q8L4Y2	Q8l4y2	arabidopsis
32	376.5	18.8	373	2	Q9SSH0	Q9ssh0	arabidopsis
33	376.5	18.8	393	2	Q9C9P8	Q9c9p8	arabidopsis
34	327	16.4	350	2	O94361	O94361	schizosacch
35	300	15.0	414	2	Q6UWP7	Q6uwp7	homo sapien
36	290	14.5	397	1	YB42_YEAST	P38226	saccharomyc
37	277.5	13.9	428	2	Q7S0V1	Q7s0v1	neurospora
38	270.5	13.5	388	2	Q6NYV8	Q6nyv8	brachydanio
39	264	13.2	409	2	Q6C336	Q6c336	yarrowia li
40	261.5	13.1	411	2	Q75CU2	Q75cu2	ashbya goss
41	246.5	12.3	397	2	Q6FQP4	Q6fqp4	candida gla
42	242	12.1	365	1	PLCE_MOUSE	Q9dle8	mus musculu
43	240	12.0	356	2	Q6NUM7	Q6num7	homo sapien
44	240	12.0	364	1	PLCE_HUMAN	Q9nuq2	homo sapien
45	239.5	12.0	396	1	YD18_YEAST	Q12185	saccharomyc
46	237.5	11.9	404	2	Q6CW53	Q6cw53	kluyveromyc
47	230	11.5	281	2	Q8SS20	Q8ss20	encephalito
48	228	11.4	368	2	Q95R12	Q95r12	caenorhabdi
49	227	11.4	420	2	Q6BL80	Q6bl80	debaryomyce
50	221	11.1	344	2	O16526	O16526	caenorhabdi
51	213.5	10.7	308	2	Q8N1Q7	Q8nlq7	homo sapien
52	212.5	10.6	143	2	Q961F9	Q961f9	drosophila
53	206	10.3	399	2	Q23087	Q23087	caenorhabdi
54	191	9.6	439	2	Q20800	Q20800	caenorhabdi
55	187	9.4	118	2	Q6AI25	Q6ai25	homo sapien
56	186	9.3	73	2	Q6PJN9	Q6pjn9	homo sapien
57	176	8.8	404	2	Q7ZT38	Q7zt38	xenopus lae
58	173.5	8.7	360	2	Q6P9I6	Q6p9i6	xenopus lae
59	172.5	8.6	304	2	Q9I5A6	Q9i5a6	pseudomonas
60	172	8.6	363	2	Q19221	Q19221	caenorhabdi
61	169.5	8.5	299	2	Q88AE0	Q88ae0	pseudomonas
62	167.5	8.4	295	2	Q88R02	Q88r02	pseudomonas
63	166.5	8.3	357	2	Q8SR20	Q8sr20	encephalito
64	166	8.3	415	2	O01882	O01882	caenorhabdi
65	163.5	8.2	292	2	Q87KC2	Q87kc2	vibrio para
66	161.5	8.1	428	2	Q95R03	Q95r03	caenorhabdi
67	160.5	8.0	300	2	Q8XQC1	Q8xqc1	ralstonia s
68	160	8.0	370	1	F34A_MOUSE	Q9lyx5	mus musculu
69	160	8.0	429	2	Q6A0A4	Q6a0a4	mus musculu
70	157	7.9	304	2	Q7QMY1	Q7qmy1	anopheles g
71	156	7.8	307	2	Q887W5	Q887w5	pseudomonas
72	152	7.6	295	2	Q9I657	Q9i657	pseudomonas
73	150	7.5	370	1	F34A_HUMAN	Q92604	homo sapien
74	147.5	7.4	271	2	Q8DDF5	Q8ddf5	vibrio vuln
75	147.5	7.4	293	2	Q7MGJ4	Q7mgj4	vibrio vuln
76	147	7.4	310	1	YIHG_ECOLI	P32129	escherichia
77	147	7.4	310	2	Q7UB62	Q7ub62	shigella fl
78	147	7.4	310	2	Q8X8H2	Q8x8h2	escherichia
79	147	7.4	318	2	Q83IV6	Q83iv6	shigella fl
80	147	7.4	318	2	Q8FBH4	Q8fbh4	escherichia
81	144.5	7.2	296	2	Q83FB3	Q83fb3	coxiella bu
82	144	7.2	302	2	Q8Z2S1	Q8z2s1	salmonella
83	143	7.2	302	2	Q8ZKU7	Q8zku7	salmonella
84	140	7.0	300	2	Q83A38	Q83a38	coxiella bu
85	139.5	7.0	294	2	Q9KVV5	Q9kvv5	vibrio chol
86	137	6.9	391	1	YT73_CAEEL	Q11087	caenorhabdi
87	134	6.7	302	2	Q8EJV9	Q8ejv9	shewanella
88	131.5	6.6	256	2	Q88B33	Q88b33	pseudomonas
89	128.5	6.4	270	2	Q8R1E1	Q8r1e1	mus musculu
90	127.5	6.4	279	2	Q9US20	Q9us20	schizosacch